

SEQUENCE LISTING

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NAKAMURA, NAMI
MIWA, TETSUYA
SEGURO, KATSUYA

<120> PROCESS FOR PRODUCING MICROBIAL TRANSGLUTAMINASE

<130> 0010-0937-0

<140> 09/109,063

<141> 1998-07-02

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<151> 1997-07-04

<160> 62

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<210> 1

<211> 331

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial
Sequence:TRANSGLUTAMINASE

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Pro	Asp	Pro	Tyr	Arg	Pro	Ser	Tyr	Gly	Arg	Ala	Glu	Thr	Val	Val	Asn
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Asn	Tyr	Ile	Arg	Lys	Trp	Gln	Gln	Val	Tyr	Ser	His	Arg	Asp	Gly	Arg
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Lys	Gln	Gln	Met	Thr	Glu	Glu	Gln	Arg	Glu	Trp	Leu	Ser	Tyr	Gly	Cys
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Val	Gly	Val	Thr	Trp	Val	Asn	Ser	Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu
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Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp	Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn
				85					90					95	
Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr	Arg	Ala	Glu	Phe	Glu	Gly	Arg	Val
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Ala	Lys	Glu	Ser	Phe	Asp	Glu	Glu	Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu
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cca gat cca tat cgt cca tct tat ggt cgt gct gaa act gtt gtt aat 96 Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn	20				25				30				
aat tat att cgt aaa tgg caa caa gtt tat tct cat cgt gat ggt cgt 144 Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg	35				40				45				
aaa caa caa atg act gaa gaa caa cgt gaa tgg ctg tct tat ggt tgc 192 Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys	50				55				60				
ggt ggt gtt act tgg gtt aac tct ggt cag tat ccg act aac cgt ctg 240 Val Gly Val Thr Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu	70				75				80				
gca ttc gct tcc ttc gat gaa gat cgt ttc aag aac gaa ctg aag aac 288 Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn	85				90				95				
ggt cgt ccg cgt tct ggt gaa act cgt gct gaa ttc gaa ggt cgt gtt 336 Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val	100				105				110				
gct aag gaa tcc ttc gat gaa gag aaa ggc ttc cag cgt gct cgt gaa 384 Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu	115				120				125				
ggt gct tct gtt atg aac cgt gct cta gag aac gct cat gat gaa tct 432 Val Ala Ser Val Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser	130				135				140				
gct tac ctg gat aac ctg aag aag gaa ctg gct aac ggt aac gat gct 480 Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala	145				150				155				
ctg cgt aac gaa gat gct cgt tct ccg ttc tac tct gct ctg cgt aac 528 Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn	165				170				175				
act ccg tcc ttc aaa gaa cgt aac ggt ggt aac cat gat ccg tct cgt 576 Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg	180				185				190				
atg aaa gct gtt atc tac tct aaa cat ttc tgg tct ggt cag gat aga 624 Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg	195				200				205				
tct tct tct gct gat aaa cgt aaa tac ggt gat ccg gat gca ttc cgt 672 Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg	210				215				220				
ccg gct ccg ggt act ggt ctg gta gac atg tct cgt gat cgt aac atc 720 Pro Ala Pro Gly Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile													

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cgt	gaa	tgg	ctg	tct	tat	ggt	tgc	ggt	ggt	ggt	act	tgg	ggt	aac	tct	305		
Arg	Glu	Trp	Leu	Ser	Tyr	Gly	Cys	Val	Gly	Val	Thr	Trp	Val	Asn	Ser			
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ggt	cag	tat	ccg	act	aac	cgt	ctg	gca	ttc	gct	tcc	ttc	gat	gaa	gat	353		
Gly	Gln	Tyr	Pro	Thr	Asn	Arg	Leu	Ala	Phe	Ala	Ser	Phe	Asp	Glu	Asp			
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cgt	ttc	aag	aac	gaa	ctg	aag	aac	ggt	cgt	ccg	cgt	tct	ggt	gaa	act	401		
Arg	Phe	Lys	Asn	Glu	Leu	Lys	Asn	Gly	Arg	Pro	Arg	Ser	Gly	Glu	Thr			
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cgt	gct	gaa	ttc	gaa	ggt	cgt	ggt	gct	aag	gaa	tcc	ttc	gat	gaa	gag	449		
Arg	Ala	Glu	Phe	Glu	Gly	Arg	Val	Ala	Lys	Glu	Ser	Phe	Asp	Glu	Glu			
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aaa	ggc	ttc	cag	cgt	gct	cgt	gaa	ggt	gct	tct	ggt	atg	aac	cgt	gct	497		
Lys	Gly	Phe	Gln	Arg	Ala	Arg	Glu	Val	Ala	Ser	Val	Met	Asn	Arg	Ala			
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cta	gag	aac	gct	cat	gat	gaa	tct	gct	tac	ctg	gat	aac	ctg	aag	aag	545		
Leu	Glu	Asn	Ala	His	Asp	Glu	Ser	Ala	Tyr	Leu	Asp	Asn	Leu	Lys	Lys			
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gaa	ctg	gct	aac	ggt	aac	gat	gct	ctg	cgt	aac	gaa	gat	gct	cgt	tct	593		
Glu	Leu	Ala	Asn	Gly	Asn	Asp	Ala	Leu	Arg	Asn	Glu	Asp	Ala	Arg	Ser			
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ccg	ttc	tac	tct	gct	ctg	cgt	aac	act	ccg	tcc	ttc	aaa	gaa	cgt	aac	641		
Pro	Phe	Tyr	Ser	Ala	Leu	Arg	Asn	Thr	Pro	Ser	Phe	Lys	Glu	Arg	Asn			
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ggt	ggt	aac	cat	gat	ccg	tct	cgt	atg	aaa	gct	ggt	atc	tac	tct	aaa	689		
Gly	Gly	Asn	His	Asp	Pro	Ser	Arg	Met	Lys	Ala	Val	Ile	Tyr	Ser	Lys			
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cat	ttc	tgg	tct	ggt	cag	gat	aga	tct	tct	tct	gct	gat	aaa	cgt	aaa	737		
His	Phe	Trp	Ser	Gly	Gln	Asp	Arg	Ser	Ser	Ser	Ala	Asp	Lys	Arg	Lys			
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tac	ggt	gat	ccg	gat	gca	ttc	cgt	ccg	gct	ccg	ggt	act	ggt	ctg	gta	785		
Tyr	Gly	Asp	Pro	Asp	Ala	Phe	Arg	Pro	Ala	Pro	Gly	Thr	Gly	Leu	Val			
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gac	atg	tct	cgt	gat	cgt	aac	atc	ccg	cgt	tct	ccg	act	tct	ccg	ggt	833		
Asp	Met	Ser	Arg	Asp	Arg	Asn	Ile	Pro	Arg	Ser	Pro	Thr	Ser	Pro	Gly			
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gaa	ggc	ttc	ggt	aac	ttc	gat	tac	ggt	tgg	ttc	ggt	gct	cag	act	gaa	881		
Glu	Gly	Phe	Val	Asn	Phe	Asp	Tyr	Gly	Trp	Phe	Gly	Ala	Gln	Thr	Glu			
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Ala	Asp	Ala	Asp	Lys	Thr	Val	Trp	Thr	His	Gly	Asn	His	Tyr	His	Ala			

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Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg				
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aac tgg tct gaa ggt tac tct gac ttc gat cgt ggt gct tac gtt atc				1025
Asn Trp Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile				
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acc ttc att ccg aaa tct tgg aac act gct ccg gac aaa gtt aaa cag				1073
Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln				
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ggg tgg ccg taatgaaagc ttggatctct aattactgga cttcacacag				1122
Gly Trp Pro				
330				
actaaaatag acatatctta tattatgtga ttttgtgaca tttcctagat gtgaggtgga				1182
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gcgcacagg tgcggttgct ggcgctata tcgccgacat caccgatggg gaagatcggg				1302
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ccgggggact gttggggcgcc atctccttgc atgcaccatt ctttgcggcg gcggtgctca				1422
acggectcaa cctactactg ggctgcttcc taatgcagga gtcgcataag ggagagcgtc				1482
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 <223> Description of Artificial Sequence:SYNTHETIC DNA

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 <210> 9
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 <210> 10
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 <211> 41
 <212> DNA
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 <210> 13
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 <400> 13
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 <210> 17
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211> 35
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 213> Artificial Sequence

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 400> 20
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 210> 21
 211> 35
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 21
 accttcgaa ttcagcacga gtttcaccag aacgc 35

 210> 22
 211> 48
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 22
 gaaggtcgtg ttgctaagga atccttcgat gaagagaaag gcttccag 48

 210> 23
 211> 48
 212> DNA
 213> Artificial Sequence

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 223> Description of Artificial Sequence:SYNTHETIC DNA

 400> 23
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 210> 24
 211> 42
 212> DNA
 213> Artificial Sequence

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 400> 24

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 210> 30
 211> 40
 212> DNA
 213> Artificial Sequence
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 223> Description of Artificial Sequence:SYNTHETIC DNA
 400> 30
 ttcgttctcc gttctactct gctctgcgta acactccgtc 40
 210> 31
 211> 39
 212> DNA
 213> Artificial Sequence
 220>
 223> Description of Artificial Sequence:SYNTHETIC DNA
 400> 31
 ctttgaagga cggagtgtta cgcagagcag agtagaacg 39
 210> 32
 211> 47
 212> DNA
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 223> Description of Artificial Sequence:SYNTHETIC DNA
 400> 32
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 210> 33
 211> 47
 212> DNA
 213> Artificial Sequence
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 223> Description of Artificial Sequence:SYNTHETIC DNA
 400> 33
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 210> 34

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 <210> 38
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210> 39
211> 48
212> DNA
213> Artificial Sequence

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223> Description of Artificial Sequence:SYNTHETIC DNA

400> 39
atcacgaga catgtctacc agaccagtac ccggagccgg acggaatg

48

210> 40
211> 35
212> DNA
213> Artificial Sequence

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223> Description of Artificial Sequence:SYNTHETIC DNA

400> 40
tgatcgtaa catcccgcgt tctccgactt ctccg

35

210> 41
211> 36
212> DNA
213> Artificial Sequence

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223> Description of Artificial Sequence:SYNTHETIC DNA

400> 41
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36

210> 42
211> 40
212> DNA
213> Artificial Sequence

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223> Description of Artificial Sequence:SYNTHETIC DNA

400> 42
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210> 43
211> 40
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213> Artificial Sequence

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 <212> DNA
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 <210> 52
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<210> 53

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<223> Description of Artificial Sequence:SYNTHETIC DNA

<400> 53

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<210> 54

<211> 38

<212> DNA

<213> Artificial Sequence

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<213> Artificial Sequence

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34

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1 5